

#9



OIPE

ENTERED

RAW SEQUENCE LISTING

DATE: 03/18/2002

PATENT APPLICATION: US/09/805,694B

TIME: 14:50:15

Input Set : A:\REVISED CORRECTED SEQUENCE LISTING BB-1432.txt

Output Set: N:\CRF3\03182002\I805694B.raw

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3 <110> APPLICANT: Kinney, Anthony
5 <120> TITLE OF INVENTION: Hypoallergenic Transgenic Soybeans
7 <130> FILE REFERENCE: BB1432 US NA
9 <140> CURRENT APPLICATION NUMBER: US/09/805,694B
10 <141> CURRENT FILING DATE: 2001-03-14
12 <150> PRIOR APPLICATION NUMBER: 60/189,823
13 <151> PRIOR FILING DATE: 2000-03-16
15 <160> NUMBER OF SEQ ID NOS: 16
17 <170> SOFTWARE: Microsoft Office 97
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1156
21 <212> TYPE: DNA
22 <213> ORGANISM: chimeric construct
24 <400> SEQUENCE: 1
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27 aacagggtgtc ttactgttgc caactatgga agagtgcgca tggacgtgtc taccataacc 180
28 acgaagaaga ggcaaaagaga cttgagattt tcaagaataa ctcgaactat atcagggaca 240
29 tgaatgcaaa cagaaaatca cccattcttc atcgtttagg attgaacaag ttgtctgaca 300
30 tcaactctca agagttcagc aaaaagtact tgcaagctcc caaggatgtg tcgcagcaaa 360
31 tcaaaatggc caacaagaaa atgaagaagg aacaatattc ttgtgacct ccacctgcat 420
32 catgggattg gaggaaaaaa ggtgtcatca cccaagtaaa gtaccaaggg ggctgtggaa 480
33 ggggttgggc gttttctgcc acgggagcca tagaagcagc acatgcaata gcaacaggag 540
34 accttgttag cctttctgaa caagaactcg tagactgtgt ggaagaaagc gaaggttctt 600
35 acaatggatg gcagtatcaa tcgttcgaat gggttttaga acatgggtggc attgccactg 660
36 atgatgatta tccttacaga gctaaagagg gtagatgcaa agccaataag atacaagaca 720
37 aggttacaat tgacggatat gaaactctaa taatgtcaga tgagagtaca gaatcagaga 780
38 cagagcaagc gttcttaagc gccatccttg agcaaccaat tagtgtctca attgatgcaa 840
39 aagattttca tttatacacc gggggaattt atgatggaga aaactgtaca agtccgtatg 900
40 ggattaatca ctttgtttta cttgtgggtt atggttcagc ggatgggtga gattactgga 960
41 tagcgaaaaa ttcattggga gaagattggg gagaagatgg ttacatttgg atccaaagaa 1020
42 acacgggtaa tttattagga gtgtgtggga tgaattattt cgcttcatac ccaaccaaag 1080
43 aggaatcaga aacactggtg tctgtctcgcg ttaaagggtc tcgaagagtt gatcactctc 1140
44 ctctttgagc ggccgc 1156
46 <210> SEQ ID NO: 2
47 <211> LENGTH: 2970
48 <212> TYPE: DNA
49 <213> ORGANISM: chimeric construct
51 <400> SEQUENCE: 2
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53 taatcagtta cttatccttc ctccatcata attaattctg gtagtctcga atgccacaac 120
54 actgactagt ctcttgatc ataagaaaaa gccaaaggaa aaaagaagac aaacacaaat 180
55 gagagtatcc ttgcatagc aatgtctaa ttcataaaat tcaaacaaaa acgcaatcac 240

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56 acacagtgga catcacttat ccactagctg aatcaggatc gccgcgtcaa gaaaaaaaaa 300
57 ctggacccca aaagccatgc acaacaacac gtactcacia aggtgtcaat cgagcagccc 360
58 aaaacattca ccaactcaac ccactcatgag ccttcacatt tgttgtttct aacccaacct 420
59 caaactcgta ttctcttcog ccacctcatt tttgtttatt tcaacaccog tcaaaactga 480
60 tgccaccccg tggccaaatg tccatgcatg ttaacaagac ctatgactat aaatatctgc 540
61 aatctcggcc cagggttttca tcatcaagaa ccagttcaat atcctagtac accgtattaa 600
62 agaatttaag atatactaac agcggcgcga tgggtttcct tgtgttgctt cttttctccc 660
63 tcttaggtct ctcttctagt tccagcatat caactcatcg ttccatattg gaccttgacc 720
64 taaccaagtt taccacacag aaacagggtg cttcactgtt ccaactatgg aagagtgagc 780
65 atggacgtgt ctaccataac cacgaagaag aggcaaagag acttgagatt ttcaagaata 840
66 actcgaacta tatcagggac atgaatgcaa acagaaaatc accccattct catcgtttag 900
67 gattgaacaa gtttgctgac atcactctc aagagttcag caaaaagtac ttgcaagctc 960
68 ccaaggatgt gtcgcagcaa atcaaaatgg ccaacaagaa aatgaagaag gaacaatatt 1020
69 cttgtgacca tccacctgca tcatgggatt ggaggaaaaa aggtgtcatc acccaagtaa 1080
70 agtaccaagg gggctgtgga aggggttggg cgttttctgc cacgggagcc atagaagcag 1140
71 cacatgcaat agcaacagga gaccttgta gcctttctga acaagaactc gtagactgtg 1200
72 tggaagaaag cgaaggttct tacaatggat ggcagtatca atcgttcgaa tgggttttag 1260
73 aacatggtgg cattgccact gatgatgatt atccttacag agctaaagag ggtagatgca 1320
74 aagccaataa gatacaagac aagggttaca ttgacggata tgaaactcta ataatgtcag 1380
75 atgagagtac agaatcagag acagagcaag cgttcttaag cgccatcctt gagcaaccaa 1440
76 ttagtgtctc aattgatgca aaagattttc atttatacac cgggggaatt tatgatggag 1500
77 aaaactgtac aagtcogtat gggattaatc actttgtttt acttgtgggt tatggttcag 1560
78 cggatggtgt agattactgg atagcgaaaa attcatgggg agaagattgg ggagaagatg 1620
79 gttacatttg gatccaaaga aacacgggta atttattagg agtgtgtggg atgaattatt 1680
80 tcgcttcata cccaaccaa gaggaatcag aaacactggt gtctgctcgc gttaaaggtc 1740
81 atcgaagagt tgatcactct cctctttgag cggccgctac atggccacgt gcatgaagta 1800
82 tgaactaaaa tgcagttagg tgtaagagct catggagagc atggaatatt gtatccgacc 1860
83 atgtaacagt ataataactg agctccatct cacttcttct atgaataaac aaaggatgtt 1920
84 atgatataat aacactctat ctatgcacct tattgttcta tgataaattt cctcttatta 1980
85 ttataaatca tctgaatcgt gacggcttat ggaatgcttc aaatagtaca aaaacaaatg 2040
86 tgtactataa gactttctaa acaattctaa ctttagcatt gtgaacgaga cataagtgtt 2100
87 aagaagacat aacaattata atggaagaag tttgtctcca tttatatatt atatattacc 2160
88 cacttatgta ttatattagg atgttaagga gacataacaa ttataaagag agaagtttgt 2220
89 atccatttat atattatata ctacccattt atatattata cttatccact tatttaatgt 2280
90 ctttataagg tttgatccat gatatttcta atattttagt tgatatgtat atgaaaggg 2340
91 actatttgaa ctctcttact ctgtataaag gttggatcat ccttaaagtg ggtctattta 2400
92 attttattgc ttcttacaga taaaaaaaaa attatgagtt ggtttgataa aatattgaag 2460
93 gatttataat aataataaat aataaataac atataatata tgtatataaa tttattataa 2520
94 tataacattt atctataaaa aagtaaatat tgtcataaat ctatacaatc gtttagcctt 2580
95 gctggacgac totcaattat ttaaacgaga gtaaacatat ttgacttttt ggttatttaa 2640
96 caaattatta tttaacacta tatgaaattt ttttttttta tcagcaaaga aataaaatta 2700
97 aattaagaag gacaatggtg tgtoccaatc cttatacaac caacttcac aagaaagtca 2760
98 agtcagagac aacaaaaaaa caagcaaagg aaatttttta atttgagttg tcttgtttgc 2820
99 tgcataattt atgcagtaaa acactacaca taacctttt agcagtagag caatggttga 2880
100 ccgtgtgctt agcttctttt attttatttt tttatcagca aagaataaat aaaataaaat 2940
101 gagacacttc agggatgttt caacaagctt 2970
103 <210> SEQ ID NO: 3
104 <211> LENGTH: 1600
105 <212> TYPE: DNA

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106 <213> ORGANISM: Glycine max
108 <400> SEQUENCE: 3
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110 caacaatggc cttccgtgat gatgaggggtg gtgataaaaa gtcacaaaaa agtttgtttt 120
111 tgatgagcaa ctccacgagg gttttcaaga ctgatgcagg ggaaatgcgt gtgctgaaaa 180
112 gccatggttg taggatattt tataggcaca tgcacattgg cttcatctct atggaaccaa 240
113 agtccttggt tgttcctcag tacctcgact ccaatctcat catattcatc cgtagagggg 300
114 aagcaaagct gggattcata tatgatgatg aactagcgga aaggagattg aagacagggg 360
115 acttgtagat gattccatct ggttcagcat tctatttggg gaacatagga gaaggtcaga 420
116 gacttcacgt tatctgcagc attgaccctt ctacaagctt gggattagag accttcaggt 480
117 ctttctatat tgggggagga gccaatctgc actcgggtgt ttctggattc gaacctgcca 540
118 tccttgaaac tgcatttaat gaatcaagaa cgggtggtaga ggaaatcttc tccaaggaac 600
119 tagatggggc aattatgttc gtggatgatt ctcatgcacc tagcttatgg actaaattcc 660
120 ttcaactgaa gaaggatgac aaagagcaac agctgaagaa aatgatgcaa gaccaagagg 720
121 aggatgagga ggagaagcaa acaagtaggt catggaggaa gctcttgga accgtatttg 780
122 ggaaggtgaa tgagaagata gagaacaaag acactgctgg tccccctgcc tcttacaacc 840
123 totacgatga caaaaaagcc gatttcaaaa acgcttatgg ttggagcaag gcactgcatg 900
124 gaggcgagta tcctccactc agcgaaccgg atattggagt tttacttgct aaactctcag 960
125 cgggatccat gttggcacct catgtgaatc caatatcaga tgagtatacc atagtgtctg 1020
126 gtggttatgg tgaactgcat atagggtatc caaacggaag caaagcaatg aaaactaaaa 1080
127 tcaacaagg ggacgtgttt gttgtgccaa gatacttccc cttctgtcaa gtagcatcaa 1140
128 gggatggacc cttagagttc tttggcttct ccacttctgc aaggaagaac aagccacagt 1200
129 ttctggctgg tgctgcgtcc cttctaagga ccttgatggg gccggagctt tcggcggcgt 1260
130 tcggagttag cgaggacacg ttgcggcgcg ctgttgatgc tcagcatgag gctgtgatac 1320
131 tgccatcagc atgggctgca ccaccggaaa atgcagggaa gctgaagatg gaagaagagc 1380
132 caaatgctat tagaagcttt gccaatgatg tggttatgga tgttttttta tttgaacact 1440
133 tgatttgga taggggttat ttggtagtgc tagtgcttag tggaattctg tgttgagttt 1500
134 tttgttcttt atatttagtt gagatgtgtg ttgtgttctt gagttgtgaa taaaaatcta 1560
135 ctttctttgt gcarraaaaa aaaaaaaaaa aaaaaaaaaa 1600
137 <210> SEQ ID NO: 4
138 <211> LENGTH: 454
139 <212> TYPE: PRT
140 <213> ORGANISM: Glycine max
142 <400> SEQUENCE: 4
143 Met ala Phe Arg Asp Asp Glu Gly Gly Asp Lys Lys Ser Pro Lys Ser
144 1 5 10 15
146 Leu Phe Leu Met Ser Asn Ser Thr Arg Val Phe Lys Thr Asp Ala Gly
147 20 25 30
149 Glu Met Arg Val Leu Lys Ser His Gly Gly Arg Ile Phe Tyr Arg His
150 35 40 45
152 Met His Ile Gly Phe Ile Ser Met Glu Pro Lys Ser Leu Phe Val Pro
153 50 55 60
155 Gln Tyr Leu Asp Ser Asn Leu Ile Ile Phe Ile Arg Arg Gly Glu Ala
156 65 70 75 80
158 Lys Leu Gly Phe Ile Tyr Asp Asp Glu Leu Ala Glu Arg Arg Leu Lys
159 85 90 95
161 Thr Gly Asp Leu Tyr Met Ile Pro Ser Gly Ser Ala Phe Tyr Leu Val
162 100 105 110
164 Asn Ile Gly Glu Gly Gln Arg Leu His Val Ile Cys Ser Ile Asp Pro

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165          115          120          125
167 Ser Thr Ser Leu Gly Leu Glu Thr Phe Gln Ser Phe Tyr Ile Gly Gly
168          130          135          140
170 Gly Ala Asn Ser His Ser Val Leu Ser Gly Phe Glu Pro Ala Ile Leu
171 145          150          155          160
173 Glu Thr Ala Phe Asn Glu Ser Arg Thr Val Val Glu Glu Ile Phe Ser
174          165          170          175
176 Lys Glu Leu Asp Gly Pro Ile Met Phe Val Asp Asp Ser His Ala Pro
177          180          185          190
179 Ser Leu Trp Thr Lys Phe Leu Gln Leu Lys Lys Asp Asp Lys Glu Gln
180          195          200          205
182 Gln Leu Lys Lys Met Met Gln Asp Gln Glu Glu Asp Glu Glu Glu Lys
183          210          215          220
185 Gln Thr Ser Arg Ser Trp Arg Lys Leu Leu Glu Thr Val Phe Gly Lys
186 225          230          235          240
188 Val Asn Glu Lys Ile Glu Asn Lys Asp Thr Ala Gly Ser Pro Ala Ser
189          245          250          255
191 Tyr Asn Leu Tyr Asp Asp Lys Lys Ala Asp Phe Lys Asn Ala Tyr Gly
192          260          265          270
194 Trp Ser Lys Ala Leu His Gly Gly Glu Tyr Pro Pro Leu Ser Glu Pro
195          275          280          285
197 Asp Ile Gly Val Leu Leu Val Lys Leu Ser Ala Gly Ser Met Leu Ala
198          290          295          300
200 Pro His Val Asn Pro Ile Ser Asp Glu Tyr Thr Ile Val Leu Ser Gly
201 305          310          315          320
203 Tyr Gly Glu Leu His Ile Gly Tyr Pro Asn Gly Ser Lys Ala Met Lys
204          325          330          335
206 Thr Lys Ile Lys Gln Gly Asp Val Phe Val Val Pro Arg Tyr Phe Pro
207          340          345          350
209 Phe Cys Gln Val Ala Ser Arg Asp Gly Pro Leu Glu Phe Phe Gly Phe
210          355          360          365
212 Ser Thr Ser Ala Arg Lys Asn Lys Pro Gln Phe Leu Ala Gly Ala Ala
213          370          375          380
215 Ser Leu Leu Arg Thr Leu Met Gly Pro Glu Leu Ser Ala Ala Phe Gly
216 385          390          395          400
218 Val Ser Glu Asp Thr Leu Arg Arg Ala Val Asp Ala Gln His Glu Ala
219          405          410          415
221 Val Ile Leu Pro Ser Ala Trp Ala Ala Pro Pro Glu Asn Ala Gly Lys
222          420          425          430
224 Leu Lys Met Glu Glu Glu Pro Asn Ala Ile Arg Ser Phe Ala Asn Asp
225          435          440          445
227 Val Val Met Asp Val Phe
228          450
230 <210> SEQ ID NO: 5
231 <211> LENGTH: 494
232 <212> TYPE: DNA
233 <213> ORGANISM: Glycine max
235 <220> FEATURE:
236 <221> NAME/KEY: unsure

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237 <222> LOCATION: (9)
238 <223> OTHER INFORMATION: n = A, C, G, or T
240 <220> FEATURE:
241 <221> NAME/KEY: unsure
242 <222> LOCATION: (388)
243 <223> OTHER INFORMATION: n = A, C, G, or T
245 <220> FEATURE:
246 <221> NAME/KEY: unsure
247 <222> LOCATION: (392)..(393)
248 <223> OTHER INFORMATION: n = A, C, G, or T
250 <220> FEATURE:
251 <221> NAME/KEY: unsure
252 <222> LOCATION: (460)
253 <223> OTHER INFORMATION: n = A, C, G, or T
255 <220> FEATURE:
256 <221> NAME/KEY: unsure
257 <222> LOCATION: (463)
258 <223> OTHER INFORMATION: n = A, C, G, or T
260 <220> FEATURE:
261 <221> NAME/KEY: unsure
262 <222> LOCATION: (468)
263 <223> OTHER INFORMATION: n = A, C, G, or T
265 <400> SEQUENCE: 5
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267 atagctgggt tgtgttcct cttccttgtt ctctttgttg ctcaagaagt tgtggtgcaa 120
268 actgaggcaa agacttgcca gaacctggct gatacataga ggggtccatg cttcaccact 180
269 ggcagctgcg atgatcactg caagaacaaa gagcacttgc tcagaggcag atgcagggac 240
270 gattttcgct gttggtgcac caaaaactgt taaatggatc cattcactcc aacgtgaaga 300
271 agatgcatgc agcgtatatt tataaaaaat acaactacta tatactatat ataataagac 360
W--> 272 tgggcgctgc atcaatgacc ctatgtanta tnnatatat tattaccgat gtcaagaact 420
W--> 273 atagatgcat gtactgtgca taacggctga gttatgtccn tangttanga ataaaaataa 480
274 agtgctgttg ttgc 494
276 <210> SEQ ID NO: 6
277 <211> LENGTH: 75
278 <212> TYPE: PRT
279 <213> ORGANISM: Glycine max
281 <400> SEQUENCE: 6
282 Met Glu Lys Lys Ser Ile Ala Gly Leu Cys Phe Leu Phe Leu Val Leu
283 1 5 10 15
285 Phe Val Ala Gln Glu Val Val Val Gln Thr Glu Ala Lys Thr Cys Glu
286 20 25 30
288 Asn Leu Ala Asp Thr Tyr Arg Gly Pro Cys Phe Thr Thr Gly Ser Cys
289 35 40 45
291 Asp Asp His Cys Lys Asn Lys Glu His Leu Leu Arg Gly Arg Cys Arg
292 50 55 60
294 Asp Asp Phe Arg Cys Trp Cys Thr Lys Asn Cys
295 65 70 75
297 <210> SEQ ID NO: 7
298 <211> LENGTH: 30

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VERIFICATION SUMMARY

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Input Set : A:\REVISED CORRECTED SEQUENCE LISTING BB-1432.txt

Output Set: N:\CRF3\03182002\I805694B.raw

L:266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5